RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/585,023*

INPUT SET: S35611.raw

> **This Raw Listing contains the General**
> **Information Section and up to the first 5 pages.**

```
 1                          SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5      (i) APPLICANT: Dalla-Favera, Riccardo
 6
 7     (ii) TITLE OF INVENTION: IDENTIFICATION OF GENES ALTERED IN
 8              MULTIPLE MYELOMA
 9
10    (iii) NUMBER OF SEQUENCES: 17
11
12     (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: Cooper & Dunham LLP
14           (B) STREET: 1185 Avenue of the Americas
15           (C) CITY: New York
16           (D) STATE: New York
17           (E) COUNTRY: U.S.A.
18           (F) ZIP: 10036
19
20      (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: Floppy disk
22           (B) COMPUTER: IBM PC compatible
23           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26     (vi) CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER:
28           (B) FILING DATE: 1-JUNE-2000
29           (C) CLASSIFICATION:
30
31   (viii) ATTORNEY/AGENT INFORMATION:
32           (A) NAME: White, John P.
33           (B) REGISTRATION NUMBER: 28,678
34           (C) REFERENCE/DOCKET NUMBER: 50995-B
35
36     (ix) TELECOMMUNICATION INFORMATION:
37           (A) TELEPHONE: (212) 278-0400
38           (B) TELEFAX: (212) 391-0525
39
40
41   (2) INFORMATION FOR SEQ ID NO:1:
42
43      (i) SEQUENCE CHARACTERISTICS:
44           (A) LENGTH: 108 amino acids
45           (B) TYPE: amino acid
46           (C) STRANDEDNESS: single
```

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/585,023*

DATE: 06/15/2000
TIME: 06:39:56

INPUT SET: S35611.raw

```
47                   (D)  TOPOLOGY: linear
48
49        (ii)  MOLECULE TYPE: peptide
50
51
52
53
54        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:1:
55
56        Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro
57        1               5                   10                  15
58
59        Gly Leu Val Trp Glu Asn Glu Glu Lys Ser Ile Phe Arg Ile Pro Trp
60                    20                  25                  30
61
62        Lys His Ala Gly Lys Gln Asp Tyr Asn Arg Glu Glu Asp Ala Ala Leu
63                35                  40                  45
64
65        Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys Phe Arg Glu Gly Ile Asp
66            50                  55                  60
67
68        Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn
69        65                  70                  75                  80
70
71        Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg Ser Gln Leu Asp Ile
72                    85                  90                  95
73
74      . Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu
75                    100                 105
76
77  (2)  INFORMATION FOR SEQ ID NO:2:
78
79        (i)  SEQUENCE CHARACTERISTICS:
80               (A)  LENGTH: 108 amino acids
81               (B)  TYPE: amino acid
82               (C)  STRANDEDNESS: single
83               (D)  TOPOLOGY: linear
84
85        (ii)  MOLECULE TYPE: peptide
86
87
88
89
90        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:2:
91
92        Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro
93        1               5                   10                  15
94
95        Gly Leu Val Trp Glu Asn Glu Glu Lys Ser Val Phe Arg Ile Pro Trp
96                    20                  25                  30
97
98        Lys His Ala Gly Lys Gln Asp Tyr Asn Arg Glu Glu Asp Ala Ala Leu
99                35                  40                  45
```

INPUT SET: S35611.raw

```
100
101      Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys Phe Arg Glu Gly Ile Asp
102          50                  55                  60
103
104      Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn
105      65                  70                  75                  80
106
107      Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg Ser Gln Leu Asp Ile
108                      85                  90                  95
109
110      Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu
111                  100                  105
112
113  (2) INFORMATION FOR SEQ ID NO:3:
114
115      (i) SEQUENCE CHARACTERISTICS:
116          (A) LENGTH: 108 amino acids
117          (B) TYPE: amino acid
118          (C) STRANDEDNESS: single
119          (D) TOPOLOGY: linear
120
121  (ii) MOLECULE TYPE: peptide
122
123
124
125
126  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
127
128      Arg Met Arg Pro Trp Leu Glu Met Gln Ile Asn Ser Asn Gln Ile Pro
129      1               5                   10                  15
130
131      Gly Leu Ile Trp Ile Asn Lys Glu Glu Met Ile Phe Gln Ile Pro Trp
132                  20                  25                  30
133
134      Lys His Ala Ala Lys His Gly Trp Asp Ile Asn Lys Asp Ala Cys Leu
135          35                  40                  45
136
137      Phe Arg Ser Trp Ala Ile His Thr Gly Arg Tyr Lys Ala Gly Glu Lys
138          50                  55                  60
139
140      Glu Pro Asp Pro Lys Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn
141      65                  70                  75                  80
142
143      Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Gln Lys Arg Asn Lys Gly
144                  85                  90                  95
145
146      Ser Ser Ala Val Arg Val Tyr Arg Met Leu Pro Pro
147                  100                 105
148
149  (2) INFORMATION FOR SEQ ID NO:4:
150
151      (i) SEQUENCE CHARACTERISTICS:
152          (A) LENGTH: 108 amino acids
```

INPUT SET: S35611.raw

```
153              (B) TYPE: amino acid
154              (C) STRANDEDNESS: single
155              (D) TOPOLOGY: linear
156
157      (ii) MOLECULE TYPE: peptide
158
159
160
161
162      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
163
164      Arg Met Arg Pro Trp Leu Glu Glu Gln Ile Asn Ser Asn Thr Ile Pro
165      1               5                   10                  15
166
167      Gly Leu Lys Trp Leu Asn Lys Glu Lys Lys Ile Phe Gln Ile Pro Trp
168                  20                  25                  30
169
170      Met His Ala Ala Arg His Gly Trp Asp Val Glu Lys Asp Ala Pro Leu
171              35                  40                  45
172
173      Phe Arg Asn Trp Ala Ile His Thr Gly Lys His Gln Pro Gly Val Asp
174          50                  55                  60
175
176      Lys Pro Asp Pro Lys Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn
177      65                  70                  75                  80
178
179      Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Lys Ser Ile Lys Lys Gly
180                      85                  90                  95
181
182      Asn Asn Ala Phe Arg Val Tyr Arg Met Leu Pro Leu
183                  100                 105

184
185  (2) INFORMATION FOR SEQ ID NO:5:
186
187      (i) SEQUENCE CHARACTERISTICS:
188              (A) LENGTH: 107 amino acids
189              (B) TYPE: amino acid
190              (C) STRANDEDNESS: single
191              (D) TOPOLOGY: linear
192
193      (ii) MOLECULE TYPE: peptide
194
195
196
197
198      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
199
200      Arg Leu Arg Gln Trp Leu Ile Glu Gln Ile Asp Ser Ser Met Tyr Pro
201      1               5                   10                  15
202
203      Gly Leu Ile Trp Glu Asn Glu Glu Lys Ser Met Phe Arg Ile Pro Trp
204                  20                  25                  30
205
```

INPUT SET: S35611.raw

```
206        Lys His Ala Gly Lys Gln Asp Tyr Asn Gln Glu Val Asp Ala Ser Ile
207            35                  40              45
208

209        Phe Lys Ala Trp Ala Val Phe Lys Gly Lys Phe Lys Glu Gly Asp Lys
210            50                  55              60
211

212        Ala Glu Pro Ala Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn Lys
213        65                  70              75                  80
214

215        Ser Pro Asp Phe Glu Glu Val Thr Asp Arg Ser Gln Leu Asp Ile Ser
216                        85                  90                  95
217

218        Glu Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu
219                    100             105
220

221   (2) INFORMATION FOR SEQ ID NO:6:
222

223        (i) SEQUENCE CHARACTERISTICS:
224            (A) LENGTH: 107 amino acids
225            (B) TYPE: amino acid
226            (C) STRANDEDNESS: single
227            (D) TOPOLOGY: linear
228

229   (ii) MOLECULE TYPE: peptide
230

231

232

233

234   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
235

236        Lys Leu Arg Asn Trp Val Val Glu Gln Val Glu Ser Gly Gln Phe Pro
237        1               5                   10                  15
238

239        Gly Val Cys Trp Asp Asp Thr Ala Lys Thr Met Phe Arg Ile Pro Trp
240                20                  25                  30
241

242        Lys His Ala Gly Lys Gln Asp Phe Arg Glu Asp Gln Asp Ala Ala Phe
243            35                  40              45
244

245        Phe Lys Ala Trp Ala Ile Phe Lys Gly Lys Tyr Lys Glu Gly Asp Thr
246            50                  55              60
247

248        Gly Gly Pro Ala Val Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn Lys
249        65                  70              75                  80
250

251        Ser Ser Glu Phe Lys Glu Val Pro Glu Arg Gly Arg Met Asp Val Ala
252                        85                  90                  95
253

254        Glu Pro Tyr Lys Val Tyr Gln Leu Leu Pro Pro
255                    100             105
256

257   (2) INFORMATION FOR SEQ ID NO:7:
258
```

****** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

```
463    (2) INFORMATION FOR SEQ ID NO:13:
464
465        (i) SEQUENCE CHARACTERISTICS:
466            (A) LENGTH: 5176 base pairs
467            (B) TYPE: nucleic acid
468            (C) STRANDEDNESS: single
469            (D) TOPOLOGY: linear
470
471        (ii) MOLECULE TYPE: other nucleic acid
472
473
474        (ix) FEATURE:
475            (A) NAME/KEY: CDS
476            (B) LOCATION: 217..1569
477
478
479        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
480
481    GCCTGACCAA CATGGTAAAA CCCCATCTCT GCTAAAACTA CAAAAAATTA GCTGGATGTG       60
482
483    GTGGCAGGGA ACCTGTCATC CCAGCTAGTT GGGAGACTGA GGCAGGAGAA TCGCTCGATC      120
484
485    TTGGGACCCA CCGCTGCCCT CAGCTCCGAG TCCAGGGCGA GTGCAGAGCA CAGCGGGCGG      180
486
487    AGGACCCCGG GCGCGGGCGC GGACGGCACG CGGGGC ATG AAC CTG GAG GGC GGC      234
488                                            Met Asn Leu Glu Gly Gly
489                                             1                   5
490
491    GGC CGA GGC GGA GAG TTC GGC ATG AGC GCG GTG AGC TGC GGC AAC GGG      282
492    Gly Arg Gly Gly Glu Phe Gly Met Ser Ala Val Ser Cys Gly Asn Gly
493             10                   15                   20
494
495    AAG CTC CGC CAG TGG CTG ATC GAC CAG ATC GAC AGC GGC AAG TAC CCC      330
496    Lys Leu Arg Gln Trp Leu Ile Asp Gln Ile Asp Ser Gly Lys Tyr Pro
497         25                   30                   35
498
499    GGG CTG GTG TGG GAG AAC GAG GAG AAG AGC ATC TTC CGC ATC CCC TGG      378
500    Gly Leu Val Trp Glu Asn Glu Glu Lys Ser Ile Phe Arg Ile Pro Trp
501     40                   45                   50
502
503    AAG CAC GCG GGC AAG CAG GAC TAC AAC CGC GAG GAG GAC GCC GCG CTC      426
504    Lys His Ala Gly Lys Gln Asp Tyr Asn Arg Glu Glu Asp Ala Ala Leu
505     55                   60                   65                   70
506
507    TTC AAG GCT TGG GCA CTG TTT AAA GGA AAG TTC CGA GAA GGC ATC GAC      474
508    Phe Lys Ala Trp Ala Leu Phe Lys Gly Lys Phe Arg Glu Gly Ile Asp
509                 75                   80                   85
```

```
510
511   AAG CCG GAC CCT CCC ACC TGG AAG ACG CGC CTG CGG TGC GCT TTG AAC        522
512   Lys Pro Asp Pro Pro Thr Trp Lys Thr Arg Leu Arg Cys Ala Leu Asn
513               90                    95                  100
514
515   AAG AGC AAT GAC TTT GAG GAA CTG GTT GAG CGG AGC CAG CTG GAC ATC        570
516   Lys Ser Asn Asp Phe Glu Glu Leu Val Glu Arg Ser Gln Leu Asp Ile
517              105                   110                 115
518
519   TCA GAC CCG TAC AAA GTG TAC AGG ATT GTT CCT GAG GGA GCC AAA AAA        618
520   Ser Asp Pro Tyr Lys Val Tyr Arg Ile Val Pro Glu Gly Ala Lys Lys
521          120                   125                 130
522
523   GGA GCC AAG CAG CTC ACC CTG GAG GAC CCG CAG ATG TCC ATG AGC CAC        666
524   Gly Ala Lys Gln Leu Thr Leu Glu Asp Pro Gln Met Ser Met Ser His
525   135               140                 145                 150
526
527   CCC TAC ACC ATG ACA ACG CCT TAC CCT TCG CTC CCA GCC CAG CAG GTT        714
528   Pro Tyr Thr Met Thr Thr Pro Tyr Pro Ser Leu Pro Ala Gln Gln Val
529               155                 160                 165
530
531   CAC AAC TAC ATG ATG CCA CCC CTC GAC CGA AGC TGG AGG GAC TAC GTC        762
532   His Asn Tyr Met Met Pro Pro Leu Asp Arg Ser Trp Arg Asp Tyr Val
533               170                 175                 180
534
535   CCG GAT CAG CCA CAC CCG GAA ATC CCG TAC CAA TGT CCC ATG ACG TTT        810
536   Pro Asp Gln Pro His Pro Glu Ile Pro Tyr Gln Cys Pro Met Thr Phe
537          185                 190                 195
538
539   GGA CCC CGC GGC CAC CAC TGG CAA GGC CCA GCT TGT GAA AAT GGT TGC        858
540   Gly Pro Arg Gly His His Trp Gln Gly Pro Ala Cys Glu Asn Gly Cys
541          200                 205                 210
542
543   CAG GTG ACA GGA ACC TTT TAT GCT TGT GCC CCA CCT GAG TCC CAG GCT        906
544   Gln Val Thr Gly Thr Phe Tyr Ala Cys Ala Pro Pro Glu Ser Gln Ala
545   215               220                 225                 230
546
547   CCC GGA GTC CCC ACA GAG CCA AGC ATA AGG TCT GCC GAA GCC TTG GCG        954
548   Pro Gly Val Pro Thr Glu Pro Ser Ile Arg Ser Ala Glu Ala Leu Ala
549               235                 240                 245
550
551   TTC TCA GAC TGC CGG CTG CAC ATC TGC CTG TAC TAC CGG GAA ATC CTC       1002
552   Phe Ser Asp Cys Arg Leu His Ile Cys Leu Tyr Tyr Arg Glu Ile Leu
553              250                 255                 260
554
555   GTG AAG GAG CTG ACC ACG TCC AGC CCC GAG GGC TGC CGG ATC TCC CAT       1050
556   Val Lys Glu Leu Thr Thr Ser Ser Pro Glu Gly Cys Arg Ile Ser His
557              265                 270                 275
558
559   GGA CAT ACG TAT GAC GCC AGC AAC CTG GAC CAG GTC CTG TTC CCC TAC       1098
560   Gly His Thr Tyr Asp Ala Ser Asn Leu Asp Gln Val Leu Phe Pro Tyr
561          280                 285                 290
562
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/585,023*

INPUT SET: S35611.raw

```
563    CCA GAG GAC AAT GGC CAC AGG AAA AAC ATT GAG AAC CTG CTG AGC CAC        1146
564    Pro Glu Asp Asn Gly His Arg Lys Asn Ile Glu Asn Leu Leu Ser His
565    295             300             305                     310
566
567    CTG GAG AGG GGC GTG GTC CTC TGG ATG GCC CCC GAC GGG CTC TAT GCG        1194
568    Leu Glu Arg Gly Val Val Leu Trp Met Ala Pro Asp Gly Leu Tyr Ala
569            315             320             325
570
571    AAA AGA CTG TGC CAG AGC ACG ATC TAC TGG GAC GGG CCC CTG GCG CTG        1242
572    Lys Arg Leu Cys Gln Ser Thr Ile Tyr Trp Asp Gly Pro Leu Ala Leu
573            330             335             340
574
575    TGC AAC GAC CGG CCC AAC AAA CTG GAG AGA GAC CAG ACC TGC AAG CTC        1290
576    Cys Asn Asp Arg Pro Asn Lys Leu Glu Arg Asp Gln Thr Cys Lys Leu
577            345             350             355
578
579    TTT GAC ACA CAG CAG TTC TTG TCA GAG CTG CAA GCG TTT GCT CAC CAC        1338
580    Phe Asp Thr Gln Gln Phe Leu Ser Glu Leu Gln Ala Phe Ala His His
581        360             365             370
582
583    GGC CGC TCC CTG CCA AGA TTC CAG GTG ACT CTA TGC TTT GGA GAG GAG        1386
584    Gly Arg Ser Leu Pro Arg Phe Gln Val Thr Leu Cys Phe Gly Glu Glu
585    375             380             385             390
586
587    TTT CCA GAC CCT CAG AGG CAA AGA AAG CTC ATC ACA GCT CAC GTA GAA        1434
588    Phe Pro Asp Pro Gln Arg Gln Arg Lys Leu Ile Thr Ala His Val Glu
589            395             400             ·405
590
591    CCT CTG CTA GCC AGA CAA CTA TAT TAT TTT GCT CAA CAA AAC AGT GGA        1482
592    Pro Leu Leu Ala Arg Gln Leu Tyr Tyr Phe Ala Gln Gln Asn Ser Gly
593            410             415             420
594
595    CAT TTC CTG AGG GGC TAC GAT TTA CCA GAA CAC ATC AGC AAT CCA GAA        1530
596    His Phe Leu Arg Gly Tyr Asp Leu Pro Glu His Ile Ser Asn Pro Glu
597            425             430             435
598
599    GAT TAC CAC AGA TCT ATC CGC CAT TCC TCT ATT CAA GAA TGAAAAATGT        1579
600    Asp Tyr His Arg Ser Ile Arg His Ser Ser Ile Gln Glu
601        440             445             450
602
603    CAAGATGAGT GGTTTTCTTT TTCCTTTTTT TTTTTTTTTT TTTTGATACG GAGATACGGG        1639
604
605    GTCTTGCTCT GTCTCCCAGG CTGGAGTGCA GTGACACAAT CTCAGCTCAC TGTGACCTCC        1699
606
607    GCCTCCTGGG TTCAAGAGAC TCTCCTGCCT CAGCCTCCCT GGTAGCTGGG ATTACAGGTG        1759
608
609    TGAGCCACTG CACCCACCCA AGACAAGTGA TTTTCATTGT AAATATTTGA CTTTAGTGAA        1819
610
611    AGCGTCCAAT TGACTGCCCT CTTACTGTTT TGAGGAACTC AGAAGTGGAG ATTTCAGTTC        1879
612
613    AGCGGTTGAG GAGAATTGCG GCGAGACAAG CATGGAAAAT CAGTGACATC TGATTGGCAG        1939
614
615    ATGAGCTTAT TTCAAAAGGA AGGGTGGCTT TGCATTTTCT TGTGTTCTGT AGACTGCCAT        1999
```

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/585,023*

INPUT SET: S35611.raw

```
616
617   CATTGATGAT CACTGTGAAA ATTGACCAAG TGATGTGTTT ACATTTACTG AAATGCGCTC   2059
618
619   TTTAATTTGT TGTAGATTAG GTCTTGCTGG AAGACAGAGA AAACTTGCCT TTCAGTATTG   2119
620
621   ACACTGACTA GAGTGATGAC TGCTTGTAGG TATGTCTGTG CCATTTCTCA GGGAAGTAAG   2179
622
623   ATGTAAATTG AAGAAGCCTC ACACGTAAAA GAAATGTATT AATGTATGTA GGAGCTGCAG   2239
624
625   TTCTTGTGGA AGACACTTGC TGAGTGAAGG AAATGAATCT TTGACTGAAG CCGTGCCTGT   2299
626
627   AGCCTTGGGG AGGCCCATCC CCCACCTGCC AGCGGTTTCC TGGTGTGGGT CCCTCTGCCC   2359
628
629   CACCCTCCTT CCCATTGGCT TTCTCTCCTT GGCCTTTCCT GGAAGCCAGT TAGTAAACTT   2419
630
631   CCTATTTTCT TGAGTCAAAA AACATGAGCG CTACTCTTGG ATGGGACATT TTTGTCTGTC   2479
632
633   CTACAATCTA GTAATGTCTA AGTAATGGTT AAGTTTTCTT GTTTCTGCAT CTTTTTGACC   2539
634
635   CTCATTCTTT AGAGATGCTA AAATTCTTCG CATAAAGAAG AAGAAATTAA GGAACATAAA   2599
636
637   TCTTAATACT TGAACTGTTG CCCTTCTGTC CAAGTACTTA ACTATCTGTT CCCTTCCTCT   2659
638
639   GTGCCACGCT CCTCTGTTTG TTTGGCTGTC CAGCGATCAG CCATGGCGAC ACTAAAGGAG   2719
640
641   GAGGAGCCGG GGACTCCCAG GCTGGAGAGC ACTGCCAGGA CCCACCACTG GAAGCAGGAT   2779
642
643   GGAGCTGACT ACGGAACTGC ACACTCAGTG GGCTGTTTCT GCTTATTTCA TCTGTTCTAT   2839
644
645   GCTTCCTCGT GCCAATTATA GTTTGACAGG GCCTTAAAAT TACTTGGCTT TTTCCAAATG   2899
646
647   CTTCTATTTA TAGAAATCCC AAAGACCTCC ACTTGCTTAA GTATACCTAT CACTTACATT   2959
648
649   TTTGTGGTTT TGAGAAAGTA CAGCAGTAGA CTGGGGCGTC ACCTCCAGGC CGTTTCTCAT   3019
650
651   ACTACAGGAT ATTTACTATT ACTCCCAGGA TTCAGCAGAA GATTGCGTTA GCTCTCAAAT   3079
652
653   GTGTGTTCCT GCTTTTCTAA TGGATATTTT AAATTCATTC AACAAGCACC TAGTAAGTGC   3139
654
655   CTGCTGTATC CCTACATTAC ACAGTTCAGC CTTTATCAAG CTTAGTGAGC AGTGAGCACT   3199
656
657   GAAACATTAT TTTTTAATGT TTAAAAAGTT TCTAATATTA AAGTCAGAAT ATTAATACAA   3259
658
659   TTAATATTAA TATTAACTAC AGAAAAGACA AACAGTAGAG AACAGCAAAA AAATAAAAAG   3319
660
661   GATCTCCTTT TTTCCCAGCC CAAATTCTCC TCTCTAAAAG TGTCCACAAG AAGGGGTGTT   3379
662
663   TATTCTTCCA ACACATTTCA CTTTTCTGTA AATATACATA AACTTAAAAA GAAAACCTCA   3439
664
665   TGGAGTCATC TTGCACACAC TTTTCATGCA GTGCTCTTTG TAGCTAAACA GTGAAGATTT   3499
666
667   ACCTCGTTCT GCTCAGAGGC CTTGCTGTGG AGCTCCACTG CCATGTACCC AGTAGGGTTT   3559
668
```

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/09/585,023*

INPUT SET: S35611.raw

```
  669   GACATTTCAT TAGCCATGCA ACATGGATAT GTATTGGGCA GCAGACTGTG TTTCGTGAAC   3619
  670
  671   TGCAGTGATG TATACATCTT ATAGATGCAA AGTATTTTGG GGTATATTAT CCTAAGGGAA   3679
  672
  673   GATAAAGATG ATATTAAGAA CTGCTGTTTC ACGGGGCCCT TACCTGTGAC CCTCTTTGCT   3739
  674
  675   GAAGAATATT TAACCCCACA CAGCACTTCA AAGAAGCTGT CTTGGAAGTC TGTCTCAGGA   3799
  676
  677   GCACCCTGTC TTCTTAATTC TCCAAGCGGA TGCTCCATTT CAATTGCTTT GTGACTTCTT   3859
  678
  679   CTTCTTTGTT TTTTTAAATA TTATGCTGCT TTAACAGTGG AGCTGAATTT TCTGGAAAAT   3919
  680
  681   GCTTCTTGGC TGGGGCCACT ACCTCCTTTC CTATCTTTAC ATCTATGTGT ATGTTGACTT   3979
  682
  683   TTTAAAATTC TGAGTGATCC AGGGTATGAC CTAGGGAATG AACTAGCTAT GGAAATAACT   4039
  684
  685   CAGGGTTAGG AATCCTAGCA CTTGTCTCAG GACTCTGAAA AGGAACGGCT TCCTCATTCC   4099
  686
  687   TTGTCTTGAT AAAGTGGAAT TGGCAAACTA GAATTTAGTT TGTACTCAGT GGACAGTGCT   4159
  688
  689   GTTGAAGATT TGAGGACTTG TTAAAGAGCA CTGGGTCATA TGGAAAAAAT GTATGTGTCT   4219
  690
  691   CCCCAGGTGC ATTTTCTTGG TTTATGTCTT GTTCTTGAGA TTTTGTATAT TTAGGAAAAC   4279
  692
  693   CTCAAGCAGT AATTAATATC TCCTGGAACA CTATAGAGAA CCAAGTGACC GACTCATTTA   4339
  694
  695   CAACTGAAAC CTAGGAAGCC CCTGAGTCCT GAGCGAAAAC AGGAGAGTTA GTCGCCCTAC   4399
  696
  697   AGAAACCCA GCTAGACTAT TGGGTATGAA CTAAAAGAG ACTGTGCCAT GGTGAGAAAA   4459
  698
  699   ATGTAAAATC CTACAGTGGA ATGAGCAGCC CTTACAGTGT TGTTACCACC AAGGGCAGGT   4519
  700
  701   AGGTATTAGT GTTTGAAAAA GCTGGTCTTT GAGCGAGGGC ATAAATACAG CTAGCCCCAG   4579
  702
  703   GGGTGGAACA ACTGTGGGAG TCTTGGGTAC TCGCACCTCT TGGCTTTGTT GATGCTCCGC   4639
  704
  705   CAGGAAGGCC ACTTGTGTGT GCGTGTCAGT TACTTTTTTA GTAACAATTC AGATCCAGTG   4699
  706
  707   TAAACTTCCG TTCATTGCTC TCCAGTCACA TGCCCCCACT TCCCCACAGG TGAAAGTTTT   4759
  708
  709   TCTGAAGTGT TGGGATTGGT TAAGGTCTTT ATTTGTATTA CGTATCTCCC CAAGTCCTCT   4819
  710
  711   GTGGCCAGCT GCATCTGTCT GAATGGTGCG TGAAGGCTCT CAGACCTTAC ACACCATTTT   4879
  712
  713   GTAAGTTATG TTTTACATGC CCCGTTTTTG AGACTGATCT CGATGCAGGT GGATCTCCTT   4939
  714
  715   GAGATCCTGA TAGCCTGTTA CAGGAATGAA GTAAAGGTCA GTTTTTTTTG TATTGATTTT   4999
  716
  717   CACAGCTTTG AGGAACATGC ATAAGAAATG TAGCTGAAGT AGAGGGGACG TGAGAGAAGG   5059
  718
  719   GCCAGGCCGG CAGGCCAACC CTCCTCCAAT GGAAATTCCC GTGTTGCTTC AAACTGAGAC   5119
  720
  721   AGATGGGACT TAACAGGCAA TGGGGTCCAC TTCCCCCTCT TCAGCATCCC CCGTACC      5176
```

INPUT SET: S35611.raw

```
722
723
```

```
822     (2)  INFORMATION FOR SEQ ID NO:15:
823
824          (i)  SEQUENCE CHARACTERISTICS:
825               (A)  LENGTH: 152 base pairs
826               (B)  TYPE: nucleic acid
827               (C)  STRANDEDNESS: single
828               (D)  TOPOLOGY: linear
829
830          (ii)  MOLECULE TYPE: DNA (genomic)
831
832
833
834
835          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:15:
836
837     TTTTCTCTAC AGTCACCTCC CTGTTTACCA AAGATAATCA CAATAAGTCC AGTTTACTTA     60
838
839     CAAAACAAGT TTAGTTATTA GAGGAAACTA AAACTTCAGG ATTCAGTCCA GATAATTTTT    120
840
841     AAAAACTCTA AAACAATGGA CAGGGCTAGA AT                                  152
842
```

```
843     (2)  INFORMATION FOR SEQ ID NO:16:
844
845          (i)  SEQUENCE CHARACTERISTICS:
846               (A)  LENGTH: 152 base pairs
847               (B)  TYPE: nucleic acid
848               (C)  STRANDEDNESS: single
849               (D)  TOPOLOGY: linear
850
851          (ii)  MOLECULE TYPE: other nucleic acid
852
853
854
855
856          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:16:
857
858     TGGGCTCGGC CTGGTGGGGC AGCCACAGCG GGACGCAGTA GTGAAAGTCC AGTTTACTTA     60
859
860     CAAAACAAGT TTAGTTATTA GAGGAAACTA AAACTTCAGG ATTCAGCAGG GCATGAGGAG    120
861
862     GCAGCTCCTC ACCCTCCCTT TCTCTTTTGT AC                                  152
863
```

```
864     (2)  INFORMATION FOR SEQ ID NO:17:
865
866          (i)  SEQUENCE CHARACTERISTICS:
867               (A)  LENGTH: 152 base pairs
868               (B)  TYPE: nucleic acid
869               (C)  STRANDEDNESS: single
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/585,023*

INPUT SET: S35611.raw

```
870                  (D) TOPOLOGY: linear
871
872          (ii) MOLECULE TYPE: DNA (genomic)
873
874
875
876
877          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
878
879  TGGGCTCGGC CTTGGTGGGG CAGCCACAGC GGGACGCAAG TAGTGAGGGC ACTCAGAACG        60
880
881  CCACTCAGCC CCGACAGGGC ACTCAGAACG CCACTCAGCC CCGACAGGCA GGGCACGAGG       120
882
883  AGGCAGCTCC TCACCCTCCC TTTCTCTTTT GT                                     152
884
```